Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 13:14:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008828.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR6008828 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008828.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 13:14:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008828.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,766,238
Mapped reads	2,227,231 / 80.51%
Unmapped reads	539,007 / 19.49%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,999 / 0.76%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	138,814 / 5.02%
Duplication rate	4.33%
Clipped reads	1,119,523 / 40.47%

2.2. ACGT Content

Number/percentage of A's	40,258,526 / 27.75%
Number/percentage of C's	27,409,202 / 18.89%
Number/percentage of T's	45,166,692 / 31.13%
Number/percentage of G's	32,046,170 / 22.09%
Number/percentage of N's	207,213 / 0.14%
GC Percentage	40.98%

2.3. Coverage

Mean	0.0469

Standard Deviation	0.6516

2.4. Mapping Quality

Mean Mapping Quality	45.35

2.5. Mismatches and indels

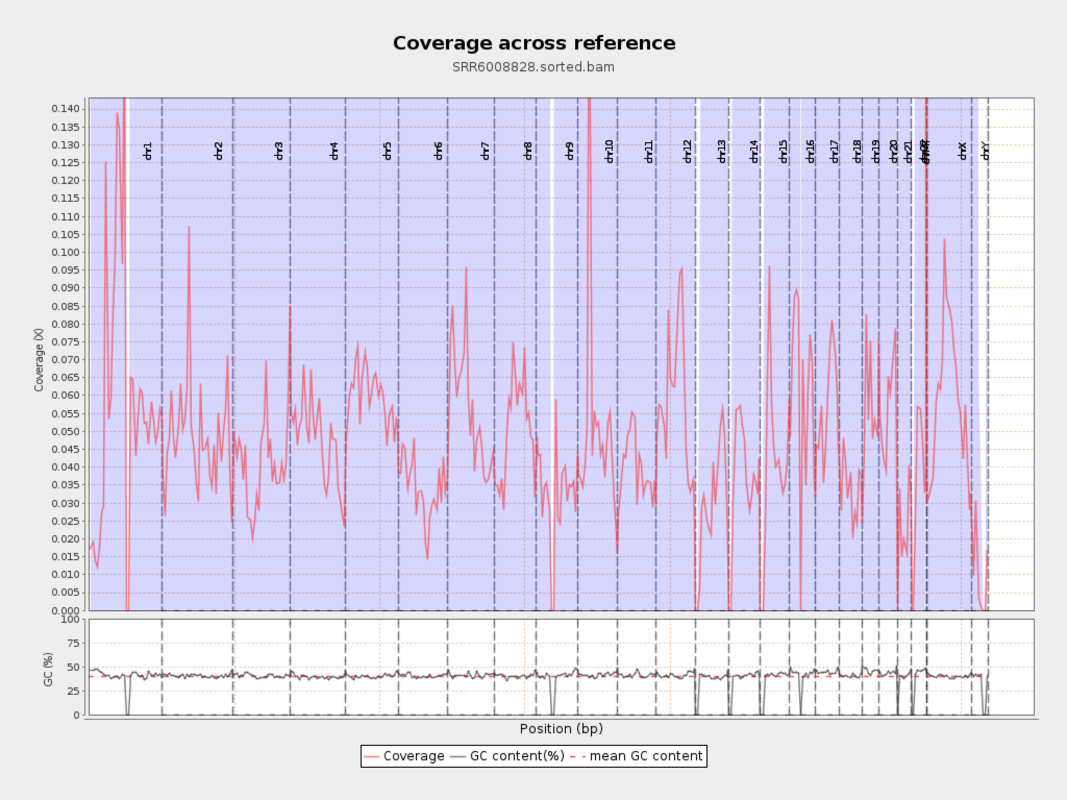
General error rate	0.95%
Mismatches	1,354,601
Insertions	10,340
Mapped reads with at least one insertion	0.46%
Deletions	50,937
Mapped reads with at least one deletion	2.26%
Homopolymer indels	44.29%

2.6. Chromosome stats

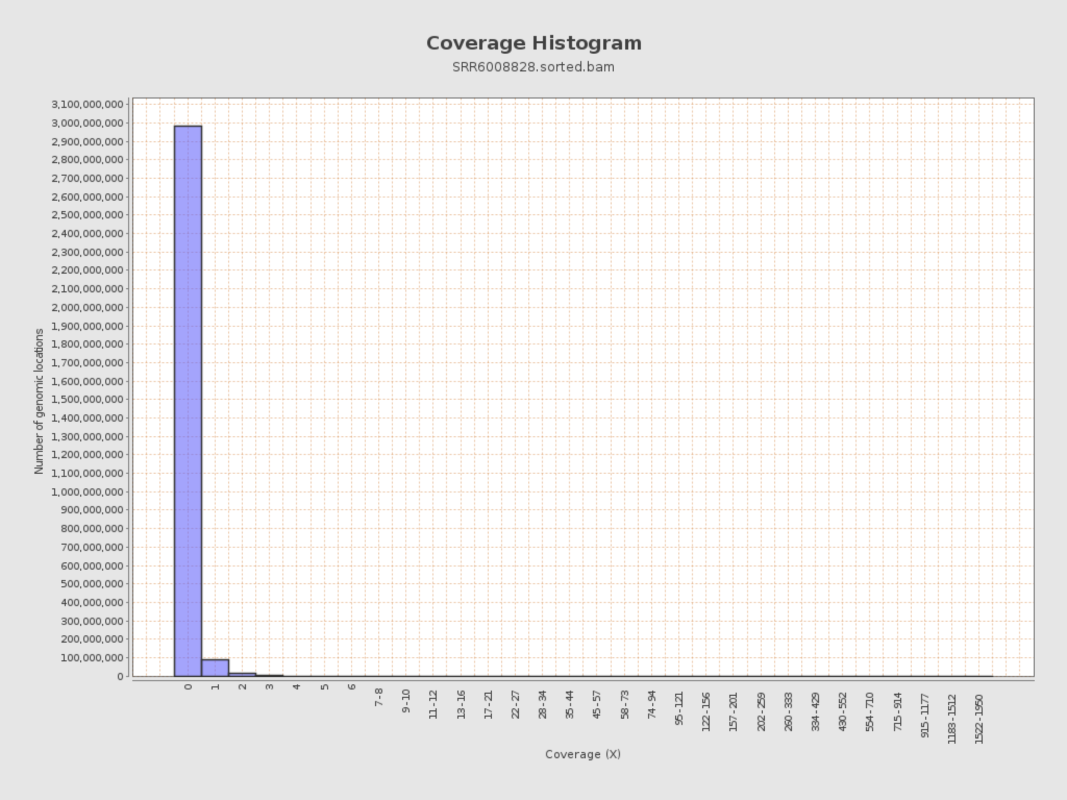
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14472392	0.0581	1.5375
chr2	243199373	11855187	0.0487	0.537
chr3	198022430	8044616	0.0406	0.3301
chr4	191154276	8988497	0.047	0.282
chr5	180915260	10826064	0.0598	0.3011
chr6	171115067	5811685	0.034	0.254
chr7	159138663	8980122	0.0564	0.6625

chr8	146364022	7445072	0.0509	0.7272
chr9	141213431	4442489	0.0315	0.4002
chr10	135534747	7027419	0.0518	1.2534
chr11	135006516	5306212	0.0393	0.3669
chr12	133851895	7963615	0.0595	0.304
chr13	115169878	3387923	0.0294	0.2076
chr14	107349540	3919498	0.0365	0.2492
chr15	102531392	4157869	0.0406	0.2487
chr16	90354753	5565772	0.0616	0.4403
chr17	81195210	4658243	0.0574	0.3344
chr18	78077248	2648487	0.0339	0.6414
chr19	59128983	3362467	0.0569	1.0053
chr20	63025520	3576235	0.0567	0.2983
chr21	48129895	1124332	0.0234	0.2092
chr22	51304566	1757008	0.0342	0.2273
chrMT	16571	209671	12.6529	8.2626
chrX	155270560	9070580	0.0584	0.3624
chrY	59373566	576301	0.0097	0.321

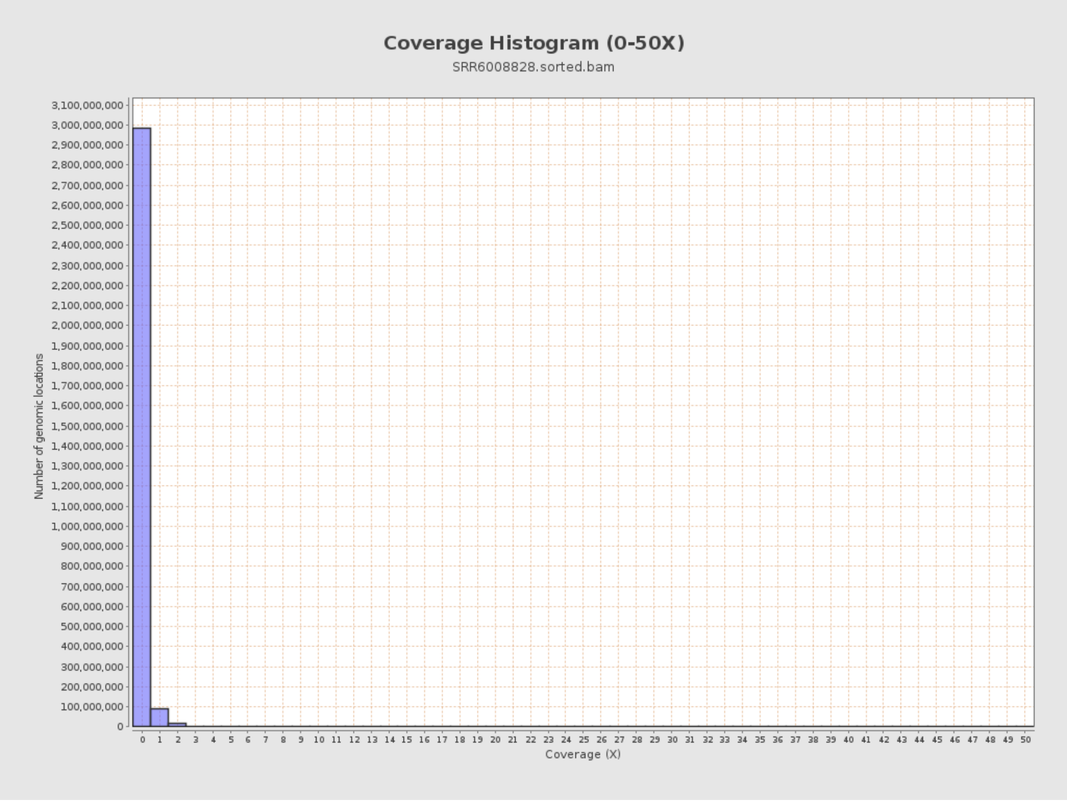
3. Results : Coverage across reference



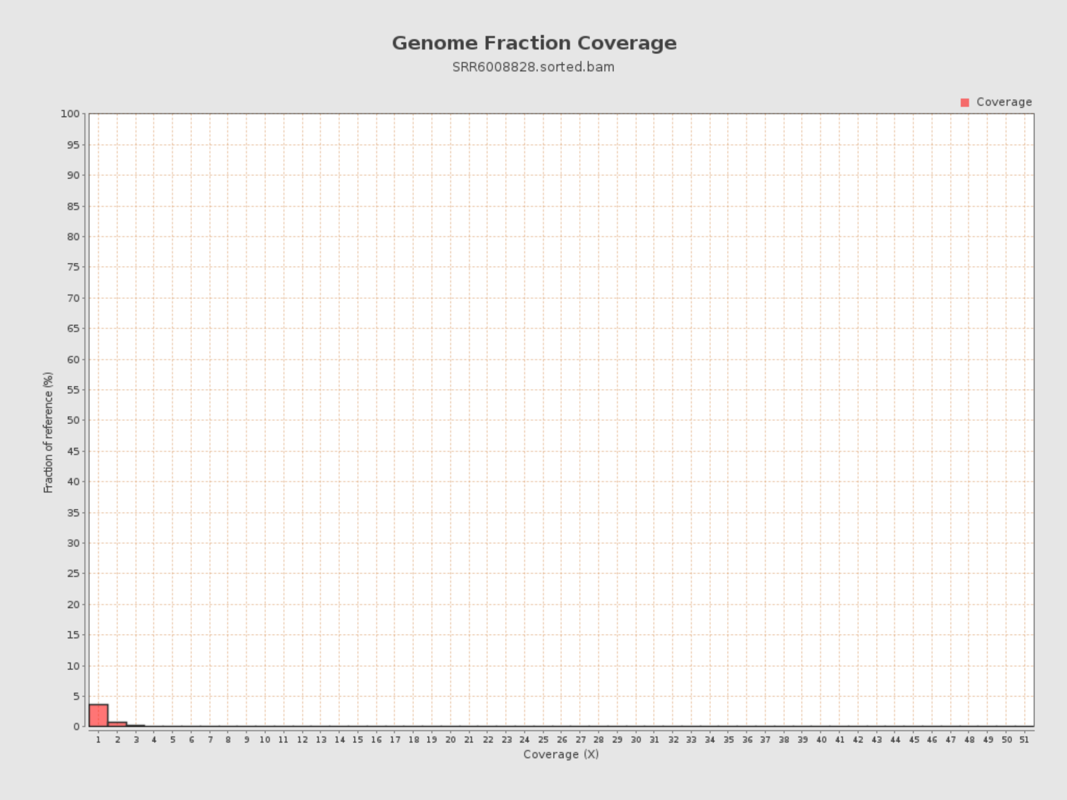
4. Results : Coverage Histogram



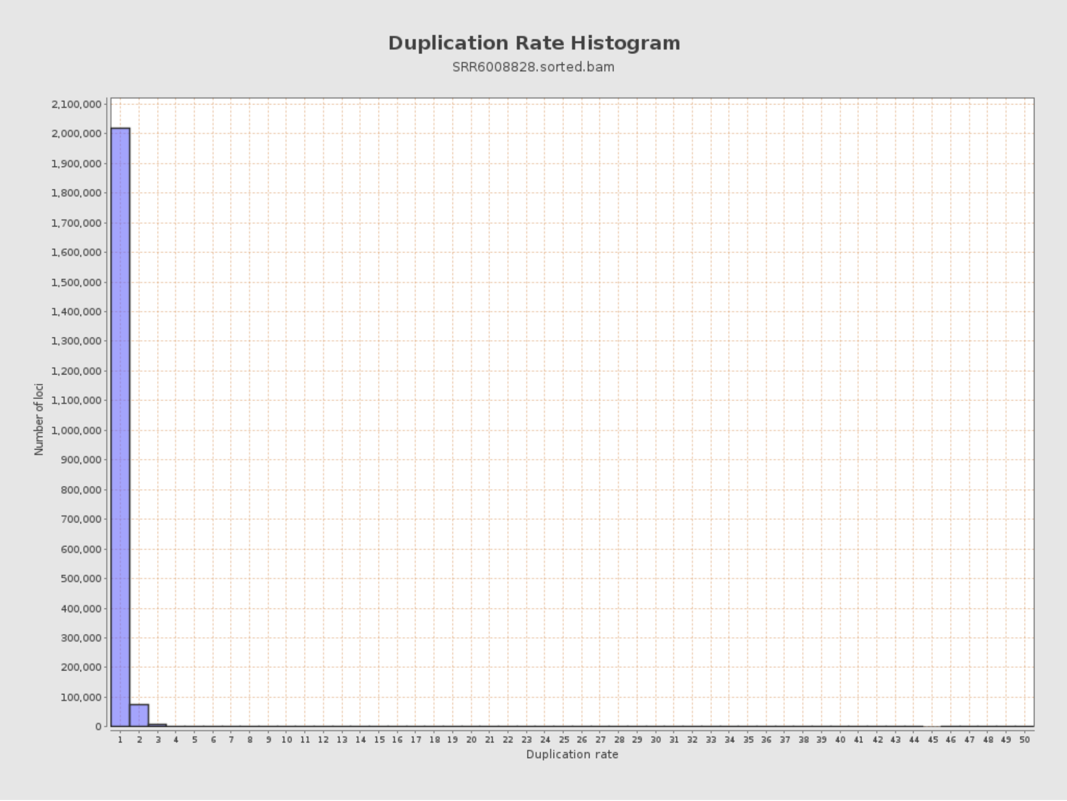
5. Results : Coverage Histogram (0-50X)



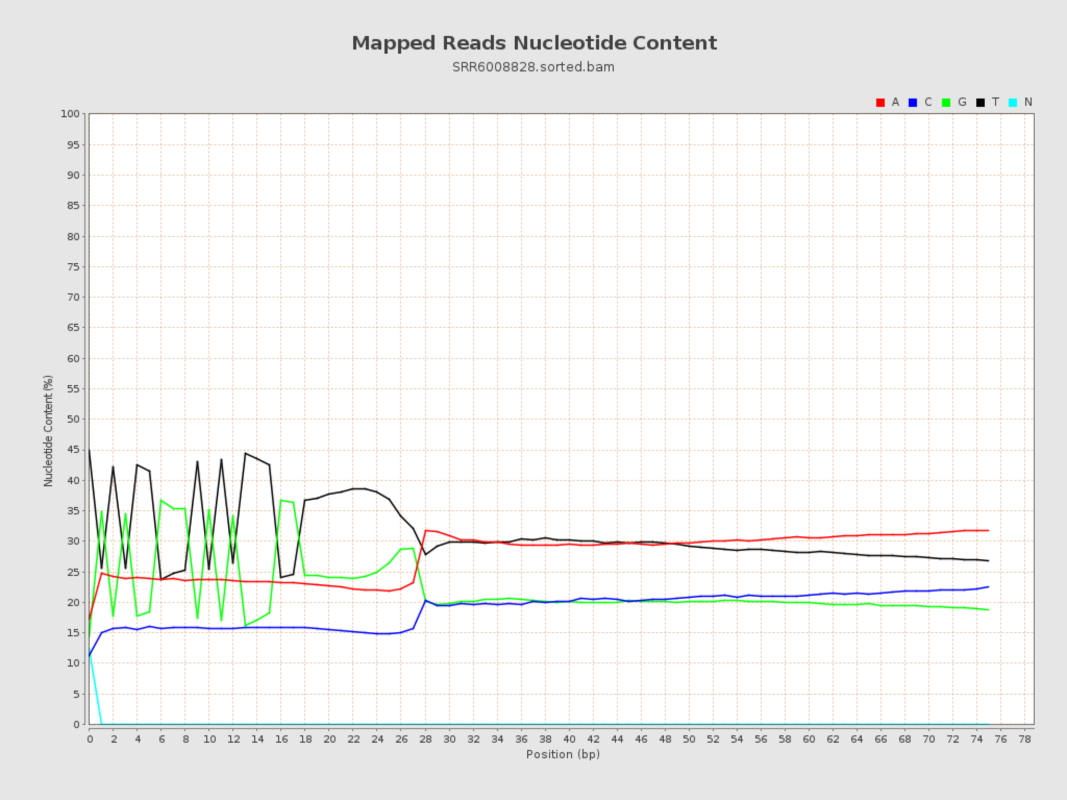
6. Results : Genome Fraction Coverage



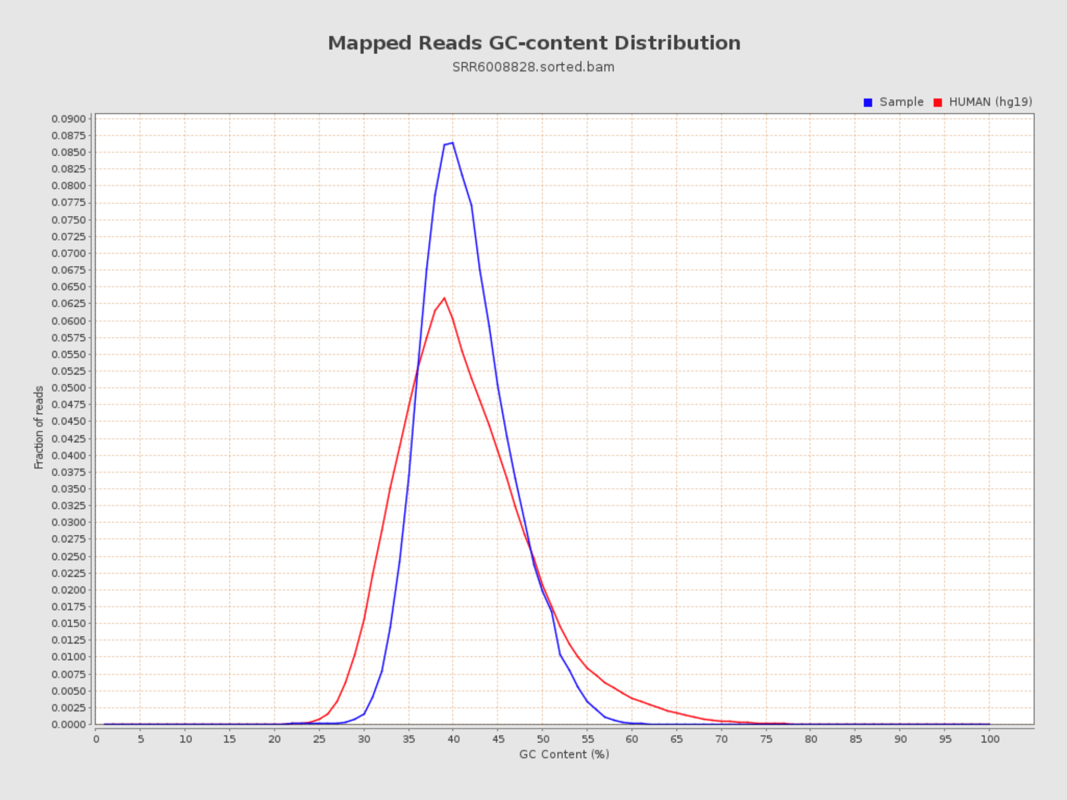
7. Results : Duplication Rate Histogram



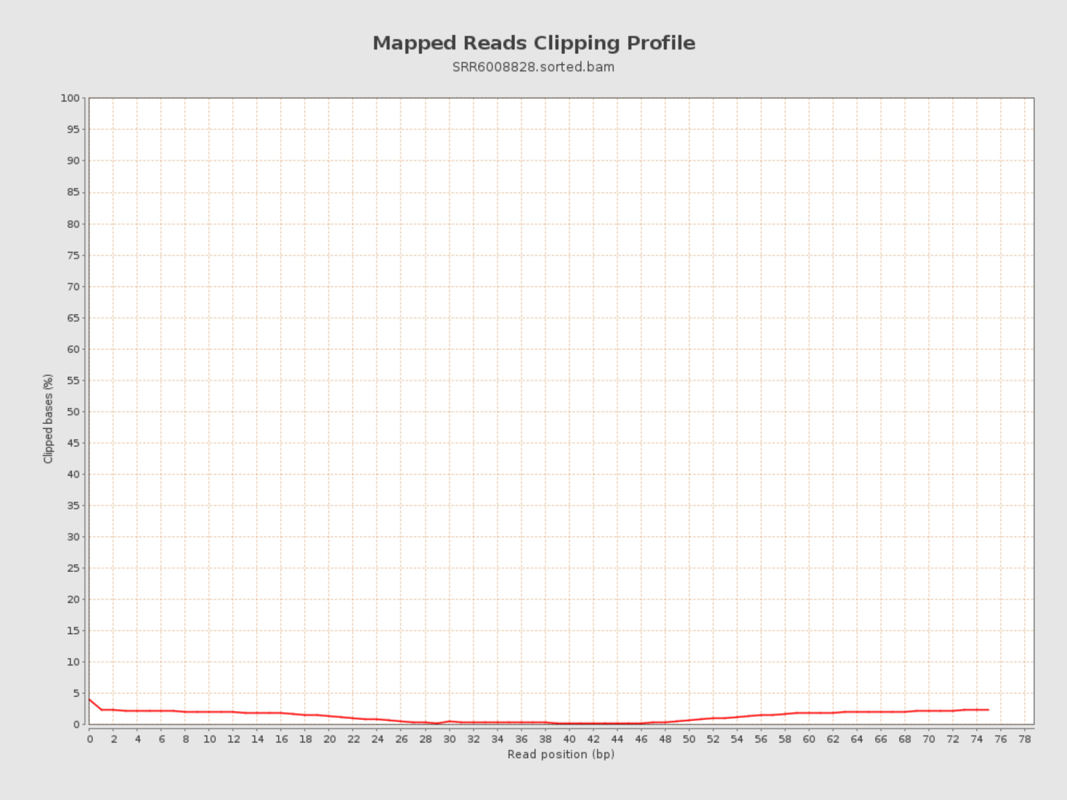
8. Results : Mapped Reads Nucleotide Content



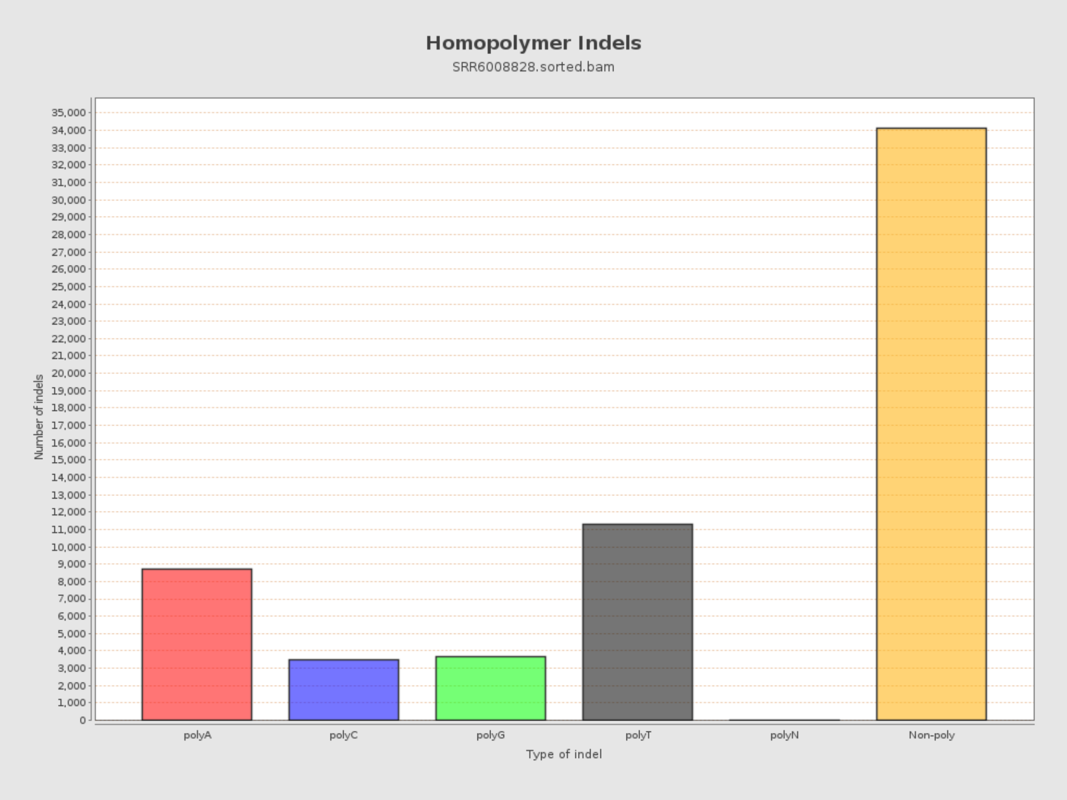
9. Results : Mapped Reads GC-content Distribution



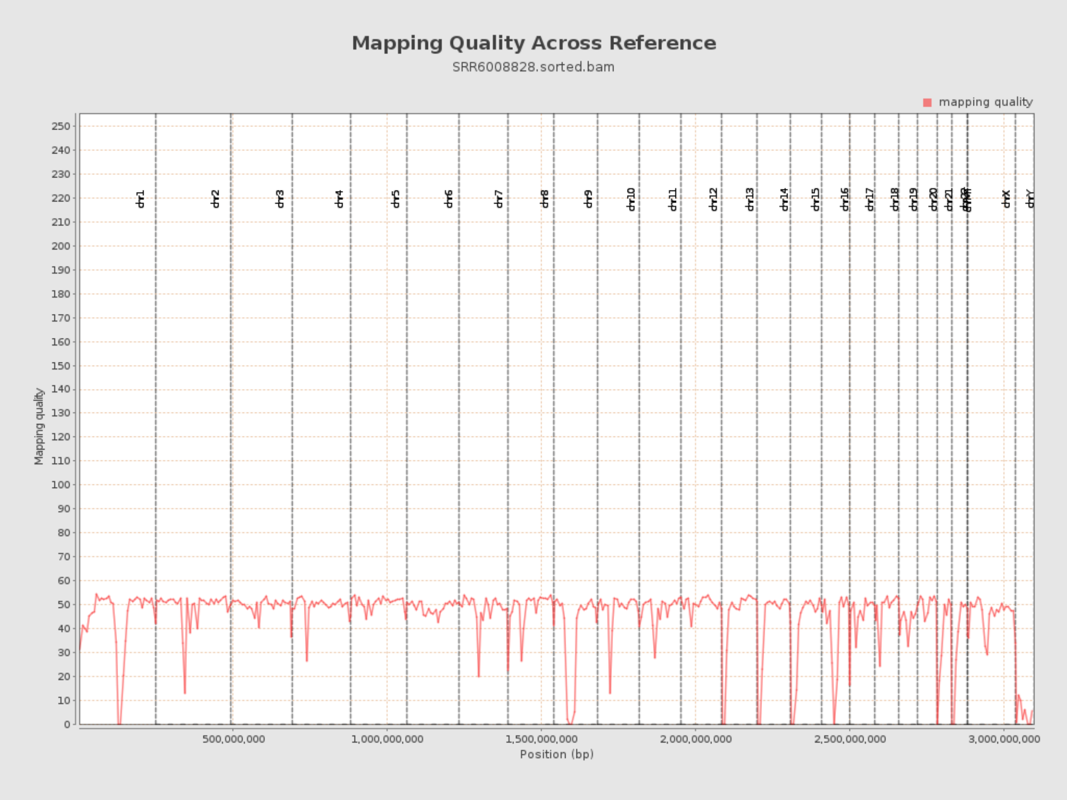
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram